

SEQUENCE LISTING

<110> Cichutek, Klaus
Engelstadter, Martin

<120> GENE TRANSFER IN HUMAN LYMPHOCYTES USING RETROVIRAL scFv CELL TARGETING

<130> 11692-006US1

<140> US 10/089,278

<141> 2002-03-26

<150> WO DE00/03444

<151> 2000-09-27

<150> DE/19946142.2

<151> 1999-09-27

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1030

<212> DNA

<213> Artificial Sequence

<220>

<223> scFv encoding sequence

<221> CDS

<222> (44)...(1030)

<400> 1

tccaccactc tgcactcaag aaagctcctg acaaccaaga aga atg gac tgt ctc	55
Met Asp Cys Leu	
1	
acc aac ctc cga tcc gct gag ggt aaa gtt gac cag gcg agc aaa atc	103
Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln Ala Ser Lys Ile	
5 10 15 20	
cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc act gcc gaa gtt	151
Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr Thr Ala Glu Val	
25 30 35	
tcg act gcc cga gcg gcc cag ccg gcc atg gcc gag gtc aag ctg cag	199
Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu Val Lys Leu Gln	
40 45 50	
cag tca ggg gct gag ctg gtg agg cct ggg gtc tca gtg aag att tcc	247
Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Val Ser Val Lys Ile Ser	
55 60 65	
tgc aag ggt tct ggc tac aca ttc act gat tat ggt atg agc tgg gtg	295
Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr Gly Met Ser Trp Val	
70 75 80	

aaa cag agt cat gca aag agt cta gag tgg att gga ctt att agt act 343
 Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly Leu Ile Ser Thr 100
 85 90 95

tac tat ggt gat cct agt tac aac cag agg ttc aag ggc aag gcc aca 391
 Tyr Tyr Gly Asp Pro Ser Tyr Asn Gln Arg Phe Lys Gly Lys Ala Thr 115
 105 110

atg act gta gac aaa tcc tcc aac aca gcc tat ttg gaa ctt gcc aga 439
 Met Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr Leu Glu Leu Ala Arg 130
 120 125

ctg aca tct gag gat tct gcc att tat tat tgt gca aga tcg gat ggt 487
 Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala Arg Ser Asp Gly 145
 135 140

aat tac ggg tat tac tat gct ttg gac tac tgg ggc caa ggc act acg 535
 Asn Tyr Gly Tyr Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr 160
 150 155

gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc 583
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly 180
 165 170 175

ggt ggc gga tcg gat atc gag ctc act cag tct cca tct tct ttg gct 631
 Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser Ser Leu Ala 195
 185 190

gtg tct cta ggg cag agg gcc acc ata tcc tgc aga gcc agt gaa agt 679
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser 210
 200 205

gtt gat agt tat ggc gat agt ttt atg cac tgg tat cag cag aaa cca 727
 Val Asp Ser Tyr Gly Asp Ser Phe Met His Trp Tyr Gln Gln Lys Pro 225
 215 220

gga cag cca ccc aaa ctc ctc atc tat cgt gca tcc aac cta gaa tct 775
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser 240
 230 235

gga gtc cct gcc agg ttc agt ggc agt ggg tct gag tca gac ttc act 823
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Glu Ser Asp Phe Thr 260
 245 250 255

ctc acc atc gat cct gtg gag gaa gat gat gct gca gtg tat tac tgt 871
 Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Ala Ala Val Tyr Tyr Cys 275
 265 270

ctg caa agt atg gaa gat ccg tac acg ttc gga ggg ggc acc aag ctg 919
 Leu Gln Ser Met Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu 290
 280 285

gaa ata aaa cgg gcg gcc gca tcg ggc tcc ggg ggc ggt ggt tct ggt 967
 Glu Ile Lys Arg Ala Ala Ala Ser Gly Ser Gly Gly Gly Ser Gly 305
 295 300

ggt ggt tct ggt ggt ggt ggt tct ggt ggt ggt ggt tct ggc gcc agc 1015
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ala Ser
310 315 320

cca gtc cag ttt atc
Pro Val Gln Phe Ile
325

1030

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<210> 2
<211> 927
<212> DNA
<213> Artificial Sequence
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<220>
<223> scFv encoding sequence

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<221> CDS
<222> (1)...(927)
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<400> 2
atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag 48
Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
1 5 10 15

gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc 96
Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
20 25 30

act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc gag 144
Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu
35 40 45

gtc aag ctg cag gag tca ggg act gaa ctt gtg aag cct ggg gct tca 192
Val Lys Leu Gln Glu Ser Gly Thr Glu Leu Val Lys Pro Gly Ala Ser
50 55 60

gtg aat ctg tct tgc aag gct tct ggc tac acc ttc acc agc tac tgg 240
Val Asn Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp
65 70 75 80

atg cac tgg ttg aag cag agg cct gga caa ggc ctt gag tgg atc gga 288
Met His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
85 90 95

gag att gat cct gtt gat agt tat act aac tac aat caa aac ttc aag 336
Glu Ile Asp Pro Val Asp Ser Tyr Thr Asn Tyr Asn Gln Asn Phe Lys
100 105 110

ggc aag gcc aca ctg act gta gac aag tcc tcc acc aca gtc tac atg 384
Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Val Tyr Met
115 120 125

cac ctc agc agc ctg aca tct gag gac tct gcg gtc tat tac tgt gca 432
 His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 130 135 140

aga aag ggc tat gct atg gac tac tgg ggc caa ggg acc aac gtc acc	480
Arg Lys Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Asn Val Thr	
145 150 155 160	
gtc tcc tca ggt gga tgc ggt tca ggc gga ggt ggc tct ggc ggt ggc	528
Val Ser Ser Gly Gly Cys Gly Ser Gly Gly Gly Ser Gly Gly Gly	
165 170 175	
gga tcg gac atc gag ctc act cag tca cca gca atc atg tct gca tct	576
Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser	
180 185 190	
cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca agt ata agt	624
Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser	
195 200 205	
tac atg cac tgg tac cag cag aag cca ggc acc tcc ccc aaa aga tgg	672
Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp	
210 215 220	
att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cgc ttc agt	720
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser	
225 230 235 240	
ggc agt ggg tct ggg acc tct tat tct ctc cca atc agc agc atg gag	768
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Pro Ile Ser Ser Met Glu	
245 250 255	
gct gaa gat gct gcc act tat tac tgc cat cag cgg agt agt tac cca	816
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro	
260 265 270	
tgg acg ttc ggt gga ggg acc aag ctg gaa ata aaa cgg gcg gcc gca	864
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala	
275 280 285	
tcg ggc tcc ggg ggc ggt ggt tct ggt ggt ggt tct ggt ggt ggt ggt	912
Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly	
290 295 300	
tct ggt ggt ggt ggt	927
Ser Gly Gly Gly Gly	
305	

<210> 3

<211> 990

<212> DNA

<213> Artificial Sequence

<220>

<223> scFv encoding sequence

<221> CDS

<222> (1)...(990)

<400> 3
 atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag 48
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln 15
 1 5 10 15
 gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc 96
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr 30
 20 25 30
 act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc cag 144
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln 45
 35 40 45
 gtg cag ctg cag cag tct ggg act gaa ctg gca aca cct ggg gcc tca 192
 Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Ala Thr Pro Gly Ala Ser 60
 50 55 60
 gtg agg atg tcc tgc aag gct tct ggc tac gcc ttt act acc tac tgg 240
 Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Tyr Trp 80
 65 70 75 80
 atg cac tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga 288
 Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly 95
 85 90 95
 tac att aat cct acc act gat tat act gac tac aat ctg aag ttc aag 336
 Tyr Ile Asn Pro Thr Thr Asp Tyr Thr Asp Tyr Asn Leu Lys Phe Lys 110
 100 105 110
 gac aag gcc aca ttg act gca gac aaa tcc tcc agt aca gcc tac atg 384
 Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met 125
 115 120 125
 caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca 432
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala 140
 130 135 140
 aga tcg ggg tgg tcc tat gct atg gac tac tgg ggg caa ggg acc acg 480
 Arg Ser Gly Trp Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr 160
 145 150 155 160
 gtc acc atc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc 528
 Val Thr Ile Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly 175
 165 170 175
 ggt ggc gga tcg gac atc gag ctc act cag tct cca gca atc atg tct 576
 Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser 190
 180 185 190
 gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt 624
 Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser 205
 195 200 205
 gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct ccc aaa 672
 Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys 220
 210 215 220

ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct gct cgc 720
 Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
 225 230 235 240

ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga 768
 Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
 245 250 255

atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg agt agt 816
 Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser
 260 265 270

tac cca ttc acg ttc ggc tcg ggc acc aag ctg gaa atc aaa cgg gcg 864
 Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
 275 280 285

gcc gca tcg ggc tcc ggg ggc ggt ggt tct ggt ggt ggt ggt tct ggt 912
 Ala Ala Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 290 295 300

ggt ggt ggt tct ggt ggt ggt ggt tct ggc gcc agc cca gtc cag ttt 960
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Ala Ser Pro Val Gln Phe
 305 310 315 320

atc ccc ctg ctt gtg ggt cta ggg att tca 990
 Ile Pro Leu Leu Val Gly Leu Gly Ile Ser
 325 330

<210> 4

<211> 946

<212> DNA

<213> Artificial Sequence

<220>

<223> scFv encoding sequence

<221> CDS

<222> (1)...(945)

<400> 4

atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag 48
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15

gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc 96
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30

act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc gag 144
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu
 35 40 45

gtc aag ctg cag cag tca ggg gct gag ctg gtg agg cct gga gct tca 192
 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
 50 55 60

gtg aag ctg tcc tgc aag act tct ggc ttc tcc ttc acc agc tac tgg 240
 Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Ser Phe Thr Ser Tyr Trp 80
 65 70 75

atg aac tgg gtg aag ctg agg cct gga caa ggc ctt gag tgg att ggc 288
 Met Asn Trp Val Lys Leu Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly 95
 85 90

atg att cat cct tcc gat agt gaa act agt tta act cag agg ttc aag 336
 Met Ile His Pro Ser Asp Ser Glu Thr Ser Leu Thr Gln Arg Phe Lys 110
 100 105

gac aag gcc aca ctg act gta gac aaa tcc tcc agc aca gcc tac atg 384
 Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met 125
 115 120

caa ctc agc agc ccg aca tct gag gac tct gcg gtc tat tac tgt gca 432
 Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala 140
 130 135

aga tct ctt tat gct aac tac ccc tcc tgg ttt act tac tgg ggc caa 480
 Arg Ser Leu Tyr Ala Asn Tyr Pro Ser Trp Phe Thr Tyr Trp Gly Gln 160
 145 150 155

ggc acc acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt 528
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly 175
 165 170

ggc tct ggc ggt ggc gga tgc gac atc gag ctc act cag tct cca acc 576
 Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr 190
 180 185

acc atg gct gca tct ccc ggg gag aag atc act atc acc tgc agt gcc 624
 Thr Met Ala Ala Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala 205
 195 200

agc tca agt ata agt tcc aat tac ttg cat tgg tat cag cag aag cca 672
 Ser Ser Ser Ile Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro 220
 210 215

gga ttc tcc cct aaa ctc ttg att tat agg aca tcc aat ctg gct tct 720
 Gly Phe Ser Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser 240
 225 230 235

gga gtc cca gct cgc ttc agt ggc agt ggg tct ggg acc tct tac tct 768
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser 255
 245 250

ctc aca att ggc acc atg gag gct gaa gat gtt gcc act tac tac tgc 816
 Leu Thr Ile Gly Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys 270
 260 265

cag cag ggt agt agt ata ccg tac acg ttc gga ggg ggg acc aag ctg 864
 Gln Gln Gly Ser Ser Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu 285
 275 280

gaa ata aaa cgg gcg gcc gca tcg ggc tcc ggg ggc ggt ggt tct ggt 912
 Glu Ile Lys Arg Ala Ala Ser Gly Ser Gly Gly Gly Gly Ser Gly
 290 295 300

ggt ggt ggt tct ggt ggt ggt ggt tct ggt ggt g 946
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 305 310 315

<210> 5
 <211> 906
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> scFv encoding sequence

<221> CDS
 <222> (1)...(906)

<400> 5 48
 atg gac tgt ctc acc aac ctc cga tcc gct gag ggt aaa gtt gac cag
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15

gcg agc aaa atc cta att ctc ctt gtg gct tgg tgg ggg ttt ggg acc 96
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30

act gcc gaa gtt tcg act gcc cga gcg gcc cag ccg gcc atg gcc cag 144
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln
 35 40 45

gta cag ctg cag cag tca gga gca gaa atg aaa aag ccc ggg gag tct 192
 Val Gln Leu Gln Gln Ser Gly Ala Glu Met Lys Lys Pro Gly Glu Ser
 50 55 60

ctg aaa atc tcc tgt aag ggt ttt gga tac gac ttt agc acc tac tgg 240
 Leu Lys Ile Ser Cys Lys Gly Phe Gly Tyr Asp Phe Ser Thr Tyr Trp
 65 70 75 80

atc gcc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag tac atg ggg 288
 Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met Gly
 85 90 95

ctc atc tat cct ggt gac tct gac acc aaa tac agc ccg tcc ttc caa 336
 Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe Gln
 100 105 110

ggc cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac ctg 384
 Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
 115 120 125

cag tgg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt gcg 432
 Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
 130 135 140

aga gtc tct gga tat tgt agt agt acc agc tgc tat gac tac tac tac 480
 Arg Val Ser Gly Tyr Cys Ser Ser Thr Ser Cys Tyr Asp Tyr Tyr Tyr 160
 145 150 155
 tac tac atg gac gtc tgg ggc cgg gga acc ctg gtc acc gtc tcg aga 528
 Tyr Tyr Met Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Arg 175
 165 170
 ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac 576
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp 190
 180 185
 atc gtg atg acc cag tct cct tcc acc ctg tct gca tct gta gga gac 624
 Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp 205
 195 200
 aga gtc acc atg act tgc cgg gcc agt cag aac att aat atc tgg ttg 672
 Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asn Ile Asn Ile Trp Leu 220
 210 215
 gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat 720
 Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr 240
 225 230 235
 aag gcg tcc act tta gag agt ggg gtc ccg tca agg ttc agc ggc agt 768
 Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 255
 245 250
 gga tct ggg aca gaa ttc act ctc acc atc agc ggc ctg cag cct gat 816
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro Asp 270
 260 265
 gat ttt gca agt tat tac tgt caa cgg tat gat agt gac tgg tcg ttc 864
 Asp Phe Ala Ser Tyr Tyr Cys Gln Arg Tyr Asp Ser Asp Trp Ser Phe 285
 275 280
 ggc caa ggg acc aag ctg gag atc aaa cgt gcg gcc gca tcg 906
 Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ser 300
 290 295

<210> 6
 <211> 329
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 6
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln 15
 1 5 10
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr 30
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu 45
 35 40 45
 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Val Ser 60
 50 55

Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr Gly 80
 65 70 75
 Met Ser Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile Gly 95
 85 90
 Leu Ile Ser Thr Tyr Tyr Gly Asp Pro Ser Tyr Asn Gln Arg Phe Lys 110
 100 105
 Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr Leu 125
 115 120
 Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala 140
 130 135
 Arg Ser Asp Gly Asn Tyr Gly Tyr Tyr Tyr Ala Leu Asp Tyr Trp Gly 160
 145 150 155
 Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly 175
 165 170
 Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro 190
 180 185
 Ser Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg 205
 195 200
 Ala Ser Glu Ser Val Asp Ser Tyr Gly Asp Ser Phe Met His Trp Tyr 220
 210 215
 Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser 240
 225 230 235
 Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Glu 255
 245 250
 Ser Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Ala Ala 270
 260 265
 Val Tyr Tyr Cys Leu Gln Ser Met Glu Asp Pro Tyr Thr Phe Gly Gly 285
 275 280
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ser Gly Ser Gly Gly 300
 290 295
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly 320
 305 310 315
 Ser Gly Ala Ser Pro Val Gln Phe Ile 325

<210> 7
 <211> 309
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> scFv

<400> 7
 Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln 15
 1 5 10
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr 30
 20 25
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu 45
 35 40
 Val Lys Leu Gln Glu Ser Gly Thr Glu Leu Val Lys Pro Gly Ala Ser 60
 50 55
 Val Asn Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp 80
 65 70 75
 Met His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly 95
 85 90

Glu Ile Asp Pro Val Asp Ser Tyr Thr Asn Tyr Asn Gln Asn Phe Lys
 100 105 110
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Val Tyr Met
 115 120 125
 His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 130 135 140
 Arg Lys Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Asn Val Thr
 145 150 155 160
 Val Ser Ser Gly Gly Cys Gly Ser Gly Gly Gly Ser Gly Gly Gly
 165 170 175
 Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
 180 185 190
 Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser
 195 200 205
 Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp
 210 215 220
 Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 225 230 235 240
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Pro Ile Ser Ser Met Glu
 245 250 255
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro
 260 265 270
 Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala
 275 280 285
 Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly
 290 295 300
 Ser Gly Gly Gly Gly
 305

<210> 8

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 8

Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln
 35 40 45
 Val Gln Leu Gln Gln Ser Gly Thr Glu Leu Ala Thr Pro Gly Ala Ser
 50 55 60
 Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Tyr Trp
 65 70 75 80
 Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
 85 90 95
 Tyr Ile Asn Pro Thr Thr Asp Tyr Thr Asp Tyr Asn Leu Lys Phe Lys
 100 105 110
 Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
 115 120 125
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 130 135 140

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Arg Ser Gly Trp Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
145          150          155          160
Val Thr Ile Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
          165          170          175
Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser
          180          185          190
Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser
          195          200          205
Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys
          210          215          220
Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
225          230          235          240
Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
          245          250          255
Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser
          260          265          270
Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
          275          280          285
Ala Ala Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
          290          295          300
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ala Ser Pro Val Gln Phe
305          310          315          320
Ile Pro Leu Leu Val Gly Leu Gly Ile Ser
          325          330

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<210> 9

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 9

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Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
1      5      10
Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
          20          25          30
Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Glu
          35          40          45
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
          50          55          60
Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Ser Phe Thr Ser Tyr Trp
          65          70          75          80
Met Asn Trp Val Lys Leu Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
          85          90          95
Met Ile His Pro Ser Asp Ser Glu Thr Ser Leu Thr Gln Arg Phe Lys
          100          105          110
Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
          115          120          125
Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
          130          135          140
Arg Ser Leu Tyr Ala Asn Tyr Pro Ser Trp Phe Thr Tyr Trp Gly Gln
145          150          155          160
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
          165          170          175

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Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr
 180 185 190
 Thr Met Ala Ala Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala
 195 200 205
 Ser Ser Ser Ile Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro
 210 215 220
 Gly Phe Ser Pro Lys Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser
 225 230 235 240
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser
 245 250 255
 Leu Thr Ile Gly Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys
 260 265 270
 Gln Gln Gly Ser Ser Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 275 280 285
 Glu Ile Lys Arg Ala Ala Ala Ser Gly Ser Gly Gly Gly Ser Gly
 290 295 300
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 305 310 315

<210> 10

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 10

Met Asp Cys Leu Thr Asn Leu Arg Ser Ala Glu Gly Lys Val Asp Gln
 1 5 10 15
 Ala Ser Lys Ile Leu Ile Leu Leu Val Ala Trp Trp Gly Phe Gly Thr
 20 25 30
 Thr Ala Glu Val Ser Thr Ala Arg Ala Ala Gln Pro Ala Met Ala Gln
 35 40 45
 Val Gln Leu Gln Gln Ser Gly Ala Glu Met Lys Lys Pro Gly Glu Ser
 50 55 60
 Leu Lys Ile Ser Cys Lys Gly Phe Gly Tyr Asp Phe Ser Thr Tyr Trp
 65 70 75 80
 Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met Gly
 85 90 95
 Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe Gln
 100 105 110
 Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
 115 120 125
 Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
 130 135 140
 Arg Val Ser Gly Tyr Cys Ser Ser Thr Ser Cys Tyr Asp Tyr Tyr Tyr
 145 150 155 160
 Tyr Tyr Met Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Arg
 165 170 175
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 180 185 190
 Ile Val Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp
 195 200 205
 Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asn Ile Asn Ile Trp Leu
 210 215 220

Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
225					230					235					240
Lys	Ala	Ser	Thr	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
				245					250					255	
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Gly	Leu	Gln	Pro	Asp
			260					265					270		
Asp	Phe	Ala	Ser	Tyr	Tyr	Cys	Gln	Arg	Tyr	Asp	Ser	Asp	Trp	Ser	Phe
		275					280					285			
Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Ala	Ser	
290						295					300				